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RAW SEQUENCE LISTING

DATE: 07/24/2001

PATENT APPLICATION: US/09/901,419

TIME: 10:53:13

Input Set : A:\Umo15311.app

Output Set: N:\CRF3\07242001\I901419.raw

ENTERED

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3 <110> APPLICANT: The Curators of the University of Missouri
5 <120> TITLE OF INVENTION: LARGE SCALE EXPRESSION AND PURIFICATION OF RECOMBINANT
6 PROTEINS
8 <130> FILE REFERENCE: UMO1531.1
C--> 10 <140> CURRENT APPLICATION NUMBER: US/09/901,419
C--> 11 <141> CURRENT FILING DATE: 2001-07-09
13 <150> PRIOR APPLICATION NUMBER: 60/218,125
14 <151> PRIOR FILING DATE: 2000-01-13
16 <160> NUMBER OF SEQ ID NOS: 2
18 <170> SOFTWARE: PatentIn Ver. 2.1
20 <210> SEQ ID NO: 1
21 <211> LENGTH: 4087
22 <212> TYPE: DNA
23 <213> ORGANISM: Bos taurus
25 <220> FEATURE:
26 <221> NAME/KEY: CDS
27 <222> LOCATION: (268)..(3180)
29 <220> FEATURE:
30 <221> NAME/KEY: sig_peptide
31 <222> LOCATION: (268)..(363)
33 <220> FEATURE:
34 <221> NAME/KEY: misc_feature
35 <222> LOCATION: (3178)
36 <223> OTHER INFORMATION: A Poly (H) affinity tag comprising 6 His residues
37 have been inserted at the C-Terminus end of the
38 coding region of the protein
40 <400> SEQUENCE: 1
41 gaattcggga gaagccatca ccccggtctc tttttcacat ccagcccatg cagaccgatc 60
43 ggccagctca accagagctg ccaactgatc tocacactta agcaaacacc accagtgagt 120
45 ggcgaacatc aactcgtgct tgaaaaaata caacttgagg ccggtttga gaagctacat 180
47 cagagtctcg agatgcgacg ctacaatctg cagttttcac tagcttccca gtagggtggg 240
49 acagttggaa ctctgccatt gccccagc atg ctg cag ttc agt ctg tca ccc acc 294
50 Met Leu Gln Phe Ser Leu Ser Pro Thr
51 1 5
53 ttg tcg atg gga ttt cac gtg ata gcc atg gtg gct ctc ttg ttt tcc 342
54 Leu Ser Met Gly Phe His Val Ile Ala Met Val Ala Leu Leu Phe Ser
55 10 15 20 25
57 cat gtg gac cat ata agt gct gag aca gaa atg gaa gga gaa ggc aac 390
58 His Val Asp His Ile Ser Ala Glu Thr Glu Met Glu Gly Glu Gly Asn
59 30 35 40
61 gag act ggc gag tgt act ggc tcc tat tac tgt aag aag ggg gtg att 438
62 Glu Thr Gly Glu Cys Thr Gly Ser Tyr Tyr Cys Lys Lys Gly Val Ile
63 45 50 55
65 tta ccc att tgg gag ccc cag gac cct tcc ttt gga gac aaa att gct 486
66 Leu Pro Ile Trp Glu Pro Gln Asp Pro Ser Phe Gly Asp Lys Ile Ala
67 60 65 70
69 aga gcg act gtg tat ttt gtg gcc atg gtc tac atg ttt ctt gga gtc 534

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70 Arg Ala Thr Val Tyr Phe Val Ala Met Val Tyr Met Phe Leu Gly Val
71      75      80      85
73 tca atc att gct gac cgg ttc atg tcc tct ata gaa gtc atc acg tct 582
74 Ser Ile Ile Ala Asp Arg Phe Met Ser Ser Ile Glu Val Ile Thr Ser
75 90      95      100      105
77 caa gag aaa gaa atc acc ata aag aaa ccc aat gga gag acc acc aag 630
78 Gln Glu Lys Glu Ile Thr Ile Lys Lys Pro Asn Gly Glu Thr Thr Lys
79      110      115
81 aca act gtg agg atc tgg aat gag aca gtg tcc aac ctg acc ttg atg 678
82 Thr Thr Val Arg Ile Trp Asn Glu Thr Val Ser Asn Leu Thr Leu Met
83      125      130      135
85 gcc ctg ggg tct tca get cca gag att ctc ott tca gta atc gag gtg 726
86 Ala Leu Gly Ser Ser Ala Pro Glu Ile Leu Leu Ser Val Ile Glu Val
87      140      145      150
89 tgt ggc cat aac ttc act gca gga gac ctt ggc cct agc acc atc gtg 774
90 Cys Gly His Asn Phe Thr Ala Gly Asp Leu Gly Pro Ser Thr Ile Val
91      155      160      165
93 ggg agt gct gca ttc aac atg ttc atc atc att gcc ctt tgt gtg tat 822
94 Gly Ser Ala Ala Phe Asn Met Phe Ile Ile Ile Ala Leu Cys Val Tyr
95 170      175      180      185
97 gtc gtc ccg gat ggg gag aca agg aag atc aag cat ctg cgt gtg ttc 870
98 Val Val Pro Asp Gly Glu Thr Arg Lys Ile Lys His Leu Arg Val Phe
99      190      195      200
101 ttt gtg aca gca gca tgg agc atc ttt gcc tat acc tgg ctt tac atc 918
102 Phe Val Thr Ala Ala Trp Ser Ile Phe Ala Tyr Thr Trp Leu Tyr Ile
103      205      210      215
105 att ttg tct gtc agc tcc cct ggg gtc gtg gag gtc tgg gaa ggt ttg 966
106 Ile Leu Ser Val Ser Ser Pro Gly Val Val Glu Val Trp Glu Gly Leu
107      220      225      230
109 ctt act ttc ttc ttc ttc ccc atc tgc gtt gtg ttt gct tgg gtg gca 1014
110 Leu Thr Phe Phe Phe Phe Pro Ile Cys Val Val Phe Ala Trp Val Ala
111      235      240      245
113 gac agg agg ctt ctg ttt tac aag tat gtc tac aag agg tat cgg gct 1062
114 Asp Arg Arg Leu Leu Phe Tyr Lys Tyr Val Tyr Lys Arg Tyr Arg Ala
115 250      255      260
117 ggc aag cag agg gga atg att att gaa cac gaa gga gac agg cca tct 1110
118 Gly Lys Gln Arg Gly Met Ile Ile Glu His Glu Gly Asp Arg Pro Ser
119      270      275      280
121 tcc aag aca gaa att gaa atg gat ggg aaa gtg gtc aat tcc cat gtt 1158
122 Ser Lys Thr Glu Ile Glu Met Asp Gly Lys Val Val Asn Ser His Val
123      285      290      295
125 gac agt ttc tta gat gga gcc ctg gtt ctg gag gtt gat gag agg gac 1206
126 Asp Ser Phe Leu Asp Gly Ala Leu Val Leu Glu Val Asp Glu Arg Asp
127      300      305      310
129 caa gat gat gaa gaa gcc agg cga gaa atg gct agg att ctg aag gaa 1254
130 Gln Asp Asp Glu Glu Ala Arg Arg Glu Met Ala Arg Ile Leu Lys Glu
131      315      320      325
133 ctc aag cag aag cat cca gag aag gaa ata gag caa tta ata gaa tta 1302
134 Leu Lys Gln Lys His Pro Glu Lys Glu Ile Glu Gln Leu Ile Glu Leu

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135 330                               335                               340                               345
137 gcc aat tac caa gtc tta agt cag cag caa aaa agt cga gcg ttt tac 1350
138 Ala Asn Tyr Gln Val Leu Ser Gln Gln Gln Lys Ser Arg Ala Phe Tyr
139                               350                               355                               360
141 cgt att caa gct acc cgc ctg atg acc gga gca ggc aac att tta aag 1398
142 Arg Ile Gln Ala Thr Arg Leu Met Thr Gly Ala Gly Asn Ile Leu Lys
143                               365                               370                               375
145 agg cat gca gca gac caa gcc agg aaa gct gtc agc atg cat gag gtc 1446
146 Arg His Ala Ala Asp Gln Ala Arg Lys Ala Val Ser Met His Glu Val
147                               380                               385                               390
149 aac acg gaa gtg gct gaa aat gac cct gtc agt aag atc ttc ttt gaa 1494
150 Asn Thr Glu Val Ala Glu Asn Asp Pro Val Ser Lys Ile Phe Phe Glu
151                               395                               400                               405
153 caa ggg aca tat cag tgt ctg gag aac tgt ggc aca gta gcc ctg acc 1542
154 Gln Gly Thr Tyr Gln Cys Leu Glu Asn Cys Gly Thr Val Ala Leu Thr
155 410                               415                               420                               425
157 att atc cgc aga ggt ggt gat ttg acc aac act gtg ttt gtt gac ttc 1590
158 Ile Ile Arg Arg Gly Gly Asp Leu Thr Asn Thr Val Phe Val Asp Phe
159                               430                               435                               440
161 aga aca gag gat ggc aca gcc aat gct gga tct gat tac gaa ttt acc 1638
162 Arg Thr Glu Asp Gly Thr Ala Asn Ala Gly Ser Asp Tyr Glu Phe Thr
163                               445                               450                               455
165 gaa gga act gtg gtc ttt aag cct ggt gag acc cag aag gaa atc aga 1686
166 Glu Gly Thr Val Val Phe Lys Pro Gly Glu Thr Gln Lys Glu Ile Arg
167                               460                               465                               470
169 gtt ggc atc att gat gat gac atc ttt gag gag gat gag aat ttc ctt 1734
170 Val Gly Ile Ile Asp Asp Asp Ile Phe Glu Glu Asp Glu Asn Phe Leu
171                               475                               480                               485
173 gtg cat ctc agc aac gtc aaa gta tct ttg gaa gcc tcg gaa gac ggc 1782
174 Val His Leu Ser Asn Val Lys Val Ser Leu Glu Ala Ser Glu Asp Gly
175 490                               495                               500                               505
177 atc ctg gaa gcc agt cat gtc tct acc ctt gct tgc ctg gga tcc ccc 1830
178 Ile Leu Glu Ala Ser His Val Ser Thr Leu Ala Cys Leu Gly Ser Pro
179                               510                               515                               520
181 tcc act gcc acc gtg act att ttt gat gat gac cat gct ggc atc ttt 1878
182 Ser Thr Ala Thr Val Thr Ile Phe Asp Asp His Ala Gly Ile Phe
183                               525                               530                               535
185 act ttt gag gaa ccg gtg act cat gtg agt gag agc att ggc atc atg 1926
186 Thr Phe Glu Glu Pro Val Thr His Val Ser Glu Ser Ile Gly Ile Met
187                               540                               545                               550
189 gag gtg aaa gtt ctg aga aca tct gga gca cgt gga aat gtt atc gtt 1974
190 Glu Val Lys Val Leu Arg Thr Ser Gly Ala Arg Gly Asn Val Ile Val
191                               555                               560                               565
193 ccc tat aag acc att gag ggg acc gcc aga ggt gga ggg gag gac ttt 2022
194 Pro Tyr Lys Thr Ile Glu Gly Thr Ala Arg Gly Gly Glu Asp Phe
195 570                               575                               580                               585
197 gag gac aca tgc gga gag ctc gag ttc cag aat gac gaa att gtc aaa 2070
198 Glu Asp Thr Cys Gly Glu Leu Glu Phe Gln Asn Asp Glu Ile Val Lys
199                               590                               595                               600

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201 aca ata tca gtc aag gta att gat gat gag gag tat gag aaa aac aag 2118
202 Thr Ile Ser Val Lys Val Ile Asp Asp Glu Glu Tyr Glu Lys Asn Lys
203 605 610 615
205 acc ttc ttc ctt gag att gga gag ccc cgc ctg gtg gag atg agt gag 2166
206 Thr Phe Phe Leu Glu Ile Gly Glu Pro Arg Leu Val Glu Met Ser Glu
207 620 625 630
209 aag aaa gcc ctg tta ttg aat gag ctt ggt ggc ttc aca ata aca ggg 2214
210 Lys Lys Ala Leu Leu Leu Asn Glu Leu Gly Gly Phe Thr Ile Thr Gly
211 635 640 645
213 aaa tac ctg tat ggc cag cct gtc ttc agg aaa gtt cat gct aga gaa 2262
214 Lys Tyr Leu Tyr Gly Gln Pro Val Phe Arg Lys Val His Ala Arg Glu
215 650 655 660 665
217 cat cca ctc ccc tct act ata atc acc atc gca gat gaa tat gat gac 2310
218 His Pro Leu Pro Ser Thr Ile Ile Thr Ile Ala Asp Glu Tyr Asp Asp
219 670 675 680
221 aag cag cca ctg acc agc aaa gag gag gaa gag agg cgc att gcg gaa 2358
222 Lys Gln Pro Leu Thr Ser Lys Glu Glu Glu Arg Arg Ile Ala Glu
223 685 690 695
225 atg ggg cgc ccc att ctg gga gag cac acc aga ctg gag gtg atc att 2406
226 Met Gly Arg Pro Ile Leu Gly Glu His Thr Arg Leu Glu Val Ile Ile
227 700 705 710
229 gaa gaa tcc tac gag ttc aag agt acc gtg gac aaa ctg att aag aag 2454
230 Glu Glu Ser Tyr Glu Phe Lys Ser Thr Val Asp Lys Leu Ile Lys Lys
231 715 720 725
233 aca aac cta gcc ctc gtg gtt ggg acg aac agc tgg aga gag cag ttc 2502
234 Thr Asn Leu Ala Leu Val Val Gly Thr Asn Ser Trp Arg Glu Gln Phe
235 730 735 740 745
237 atc gag gcg atc act gtc agt gct ggg gaa gat gac gat gac gac gaa 2550
238 Ile Glu Ala Ile Thr Val Ser Ala Gly Glu Asp Asp Asp Asp Glu
239 750 755 760
241 tgt ggg gag gag aag ctg ccc tcc tgt ttt gac tac gtg atg cac ttt 2598
242 Cys Gly Glu Glu Lys Leu Pro Ser Cys Phe Asp Tyr Val Met His Phe
243 765 770 775
245 ctg act gtg ttc tgg aag gtc ctc ttc gcc ttt gtc ccc ccg aca gag 2646
246 Leu Thr Val Phe Trp Lys Val Leu Phe Ala Phe Val Pro Pro Thr Glu
247 780 785 790
249 tac tgg aac gcc tgg gcg tgt ttc atc gtc tcc atc ctc atg atc gcc 2694
250 Tyr Trp Asn Gly Trp Ala Cys Phe Ile Val Ser Ile Leu Met Ile Gly
251 795 800 805
253 cta ctg acg gct ttc att gga gac ctc gct tcc cac ttc gcc tgc acc 2742
254 Leu Leu Thr Ala Phe Ile Gly Asp Leu Ala Ser His Phe Ala Cys Thr
255 810 815 820 825
257 atc gcc ctg aag gat tcc gtg acc gcg gtg gtg ttc gtt gcg ctt gga 2790
258 Ile Ala Leu Lys Asp Ser Val Thr Ala Val Val Phe Val Ala Leu Gly
259 830 835 840
261 acc tca gtg cca gac aca ttt gca agc aaa gtg gcc gcc acc cag gac 2838
262 Thr Ser Val Pro Asp Thr Phe Ala Ser Lys Val Ala Ala Thr Gln Asp
263 845 850 855
265 cag tat gcg gat gca tcc ata ggt aac gtc aca ggc agc aac gcg gtg 2886

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266 Gln Tyr Ala Asp Ala Ser Ile Gly Asn Val Thr Gly Ser Asn Ala Val
267      860      865      870
269 aac gtc ttc ctg ggc atc ggt gtg gcc tgg tcc atc gcc gcc atc tac 2934
270 Asn Val Phe Leu Gly Ile Gly Val Ala Trp Ser Ile Ala Ala Ile Tyr
271      875      880      885
273 cac gcg gcc aac ggg gaa cag ttc aaa gtg tcc cct ggc acg cta gct 2982
274 His Ala Ala Asn Gly Glu Gln Phe Lys Val Ser Pro Gly Thr Leu Ala
275      890      895      900      905
277 ttt tct gtc act ctc ttc acc att ttt gct ttc atc aat gtg ggg gtg 3030
278 Phe Ser Val Thr Leu Phe Thr Ile Phe Ala Phe Ile Asn Val Gly Val
279      910      915      920
281 ctg ctg tat cgg cgg agg cca gaa att gga ggt gag ctg ggt ggg ccc 3078
282 Leu Leu Tyr Arg Arg Arg Pro Glu Ile Gly Gly Glu Leu Gly Gly Pro
283      925      930      935
285 cgg act gcc aag ctc ctc aca tcc tgc ctc ttt gtg ctc ctg tgg ctc 3126
286 Arg Thr Ala Lys Leu Leu Thr Ser Cys Leu Phe Val Leu Leu Trp Leu
287      940      945      950
289 ttg tac att ttc ttc tcc tcc ctg gag gcc tac tgc cac ata aaa ggc 3174
290 Leu Tyr Ile Phe Phe Ser Ser Leu Glu Ala Tyr Cys His Ile Lys Gly
291      955      960      965
293 ttc taa aggaacaatc agatgtagta aatttatata tatatacata tatatatata 3230
294 Phe
295 970
297 cataaaaatt atgtataatg aacagaggaa actggcattt gtcatgtcca cccacctgct 3290
299 gatggaatcc agcttcaaga gcagactctg tactagggcc ggagagagaa gccatocact 3350
301 ccggtttccc agggcgcttc gtcttgttga accaggcatg gagcgaggcc catcttttacg 3410
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313 tattactaaa ttatcatgct tatctctgga gtgggagcag aggtgaagtc ctccctccaa 3770
315 gaagaaacag gggagctgga atggagccaa gaagatcat ggttctagat acagtctgat 3830
317 gtttaaagat acatcgtctc ctggcacccc tgttcaacag gtacaaaaac aacatgccta 3890
319 gatccccagg aacgcacaaa gtcctttctt atctcttcag cgctggaactg tgattagcaa 3950
321 ggccctgatt ctgatgtttc acaccgcgtg atcccccagc cctcccactcc caaaccctt 4010
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328 <210> SEQ ID NO: 2
329 <211> LENGTH: 970
330 <212> TYPE: PRT
331 <213> ORGANISM: Bos taurus
333 <400> SEQUENCE: 2
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335      1      5      10      15
336 Ile Ala Met Val Ala Leu Leu Phe Ser His Val Asp His Ile Ser Ala
337      20      25      30
338 Glu Thr Glu Met Glu Gly Glu Gly Asn Glu Thr Gly Glu Cys Thr Gly
339      35      40      45

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L:10 M:270 C: Current Application Number differs, Replaced Application Number

L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date